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SEQUENCE LISTING

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YAMAGUCHI, Nozomi  
MITSUI, Shinichi

<120> NOVEL SERINE PROTEASE BSSP6

<130> UEMURA=4

<140> 09/856,320

<141> 2001-05-21

<150> JP 10-347802

<151> 1998-11-20

<160> 41

<170> PatentIn version 3.1

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Met Gln

agg ttg agg tgg ctg cgg gac tgg aag tca tcg ggc aga ggt ctc aca 166  
Arg Leu Arg Trp Leu Arg Asp Trp Lys Ser Ser Gly Arg Gly Leu Thr  
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gca gcc aag gaa cct ggg gcc cgc tcc tcc ccc ctc cag gcc atg agg 214  
Ala Ala Lys Glu Pro Gly Ala Arg Ser Ser Pro Leu Gln Ala Met Arg  
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Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly  
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ctc	atc	gcc	ccc	aga	tgg	ctc	ctg	aca	gca	gcc	cac	tgc	ctc	aag	ccc	406	
Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	Ala	His	Cys	Leu	Lys	Pro	45	
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cgc	tac	ata	gtt	cac	ctg	ggg	cag	cac	aac	ctc	cag	aag	gag	gag	ggc	454	
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tgt	gag	cag	acc	cgg	aca	gcc	act	gag	tcc	ttc	ccc	cac	ccc	ggc	ttc	502	
Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	75	
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Asn	Asn	Ser	Leu	Pro	Asn	Lys	Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	90	
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Lys	Met	Ala	Ser	Pro	Val	Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	105	
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Leu	Ser	Ser	Arg	Cys	Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	125	
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tgg	ggc	agc	acg	tcc	agc	ccc	cag	tta	cgc	ctg	cct	cac	acc	ttg	cga	694	
Trp	Gly	Ser	Thr	Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	140	
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Cys	Ala	Asn	Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	155	
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Pro	Gly	Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	170	
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Gly	Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	185	
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cag	tct	ctt	caa	ggc	att	atc	tcc	tgg	ggc	cag	gat	ccg	tgt	gcg	atc	886	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	Ile	205	
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acc	cga	aag	cct	ggt	gtc	tac	acg	aaa	gtc	tgc	aaa	tat	gtg	gac	tgg	934	
Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	Asp	Trp	220	
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Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn										
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actctgggaa	tgacaacacc	tggtttggtc	tctgttggtat	cccagcccc	aaagacagct												1228

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Lys Pro Arg Tyr Ile Val His Leu Gly Gln (His Asn Leu Gln Lys Glu  
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Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro  
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Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met  
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Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro  
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Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile  
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Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr  
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Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn  
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Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys  
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aag agt gac tgg aaa tta tct aca gaa acc agg gaa cct ggc gcc cgc 162  
Lys Ser Asp Trp Lys Leu Ser Thr Glu Thr Arg Glu Pro Gly Ala Arg  
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cct gcc cta ctc cag gcc agg atg att ctc cga ctc att gca ctt gct 210  
Pro Ala Leu Leu Gln Ala Arg Met Ile Leu Arg Leu Ile Ala Leu Ala  
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ctg gta aca ggg cac gta ggg gga gag acg agg atc atc aag ggt tat 258  
Leu Val Thr Gly His Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Tyr  
-10 -5 -1 1 5  
gag tgc agg cct cac tca cag cca tgg cag gtg gcc ctc ttt cag aag 306  
Glu Cys Arg Pro His Ser Gln Pro Trp Gln Val Ala Leu Phe Gln Lys  
10 15 20  
aca cgg ctt ctc tgt ggg gca acc ctc atc gcc ccc aaa tgg ctc ctg 354  
Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro Lys Trp Leu Leu

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cac aat cta gag aag aca gac ggc tgt gag cag agg cgg atg gcc act His Asn Leu Glu Lys Thr Asp Gly Cys Glu Gln Arg Arg Met Ala Thr 55 60 65			450
gag tcc ttc ccc cac ccc gac ttc aac aac agc ctc ccc aac aaa gac Glu Ser Phe Pro His Pro Asp Phe Asn Asn Ser Leu Pro Asn Lys Asp 70 75 80 85			498
cac cgg aat gac ata atg ctt gtg aag atg tgc tct ccc gtc ttc ttt His Arg Asn Asp Ile Met Leu Val Lys Met Ser Ser Pro Val Phe Phe 90 95 100			546
acc cga gct gtg cag cca ctc acc ctg tcc cca cac tgt gtc gct gca Thr Arg Ala Val Gln Pro Leu Thr Leu Ser Pro His Cys Val Ala Ala 105 110 115			594
ggc acc agc tgc ctc att tct gga tgg ggc acc acg tcc agc ccc cag Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr Thr Ser Ser Pro Gln 120 125 130			642
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Leu Phe Gln Lys Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro  
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Lys Trp Leu Leu Thr Ala Ala His Cys Arg Lys Pro His Tyr Val Ile  
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Leu Leu Gly Glu His Asn Leu Glu Lys Thr Asp Gly Cys Glu Gln Arg  
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Arg Met Ala Thr Glu Ser Phe Pro His Pro Asp Phe Asn Asn Ser Leu  
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Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ser Ser  
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Pro Val Phe Phe Thr Arg Ala Val Gln Pro Leu Thr Leu Ser Pro His  
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Cys Val Ala Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr Thr  
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Ser Ser Pro Gln Leu Arg Leu Pro His Ser Leu Arg Cys Ala Asn Val  
 130 135 140 145

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 150 155 160

Thr Asp Thr Met Leu Cys Ala Ser Val Arg Lys Glu Gly Lys Asp Ser  
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Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Ser Leu Gln  
180 185 190

Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala Val Thr Arg Lys Pro  
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Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro  
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Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr  
15 20 25  
  
ctc atc gcc ccc aga tgg ctc ctg aca gca gcc cac tgc ctc aag ccg 248  
Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro  
30 35 40 45  
  
tgg gtg tca ctc acc tct ccc acc cat gtc tcc ccc gac ctt tcc tcc 296  
Trp Val Ser Leu Thr Ser Pro Thr His Val Ser Pro Asp Leu Ser Ser  
50 55 60  
  
tcc aac tac tgt ctc tcc cac ctc agc cgc tac ata gtt cac ctg ggg 344  
Ser Asn Tyr Cys Leu Ser His Leu Ser Arg Tyr Ile Val His Leu Gly  
65 70 75

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gac cac cgc aat gac atc atg ctg gtg aag atg gca tgc cca gtc tcc Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val Ser 110 115 120 125	488
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gct ggc acc agc tgc ctc att tcc ggc tgg ggc agc acg tcc agc ccc Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr Ser Ser Pro 145 150 155	584
cag tta cgc ctg cct cac acc ttg cga tgc gcc aac atc acc atc att Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn Ile Thr Ile Ile 160 165 170	632
gag cac cag aag tgt gag aac gcc tac ccc ggc aac atc aca gac acc Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly Asn Ile Thr Asp Thr 175 180 185	680
atg gtg tgt gcc agc gtg cag gaa ggg ggc aag gac tcc tgc cag ggt Met Val Cys Ala Ser Val Gln Glu Gly Gly Lys Asp Ser Cys Gln Gly 190 195 200 205	728
gac tcc ggg ggc cct ctg gtc tgt aac cag tct ctt caa ggc att atc Asp Ser Gly Gly Pro Leu Val Cys Asn Gln Ser Leu Gln Gly Ile Ile 210 215 220	776
tcc tgg ggc cag gat ccg tgt gcg atc acc cga aag cct ggt gtc tac Ser Trp Gly Gln Asp Pro Cys Ala Ile Thr Arg Lys Pro Gly Val Tyr 225 230 235	824
acg aaa gtc tgc aaa tat gtg gac tgg atc cag gag acg atg aag aac Thr Lys Val Cys Lys Tyr Val Asp Trp Ile Gln Glu Thr Met Lys Asn 240 245 250	872
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Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu  
30 35 40

Lys Pro Trp Val Ser Leu Thr Ser Pro Thr His Val Ser Pro Asp Leu  
45 50 55

Ser Ser Ser Asn Tyr Cys Leu Ser His Leu Ser Arg Tyr Ile Val His  
60 65 70 75

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80 85 90

Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro  
95 100 105

Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro  
110 115 120

Val Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys  
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Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr Ser  
140 145 150 155

Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn Ile Thr  
160 165 170

Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly Asn Ile Thr  
175 180 185

Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly Lys Asp Ser Cys  
190 195 200

Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gln Ser Leu Gln Gly  
205 210 215

Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala Ile Thr Arg Lys Pro Gly  
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Lys Asn Asn

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<210> 9  
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 <400> 9  
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<210> 10  
 <211> 27  
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 SecTrypHis/Neurosin

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 <223> Designed oligonucleotide primer designated as hBSSP6F4 to amplify  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 or human BSSP6 (reverse)  
  
 <400> 23  
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 <210> 24  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Designed oligonucleotide primer designated as hBSSP6R2 for RACE f  
 or human BSSP6 (reverse)  
  
 <400> 24  
 atggtgtctg tgatgttgcc 20  
  
 <210> 25  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Designed oligonucleotide primer designated as hBSSP6R3/P to ampli  
 fy full-length human BSSP6-encoding mRNA (reverse)  
  
 <400> 25  
 aactgcagga accaaacacc aagtgg 26

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<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP6F1 for RACE f
      or mouse BSSP6 (forward)

<400> 26
cgacttcaac aacagcctcc
                                                    20

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designated oligonucleotide primer designated as mBSSP6F2 for RACE
      for mouse BSSP6 (forward)

<400> 27
cttctttacc cgagctgtgc
                                                    20

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP6F3 to amplify
      full-length mouse prostate BSSP6-encoding mRNA (forward)

<400> 28
taagctagga gaactgaggc
                                                    20

<210> 29
<211> 18
<212> DNA
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<220>
<223> Designed oligonucleotide primer designated as mBSSP6F4 to amplify
      mature mouse BSSP6-encoding region (forward)

<400> 29
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                                                    18

<210> 30
<211> 19
<212> DNA
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<220>
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<400> 30  
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<210> 31  
<211> 20  
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<220>  
<223> Designed oligonucleotide primer designated as mBSSP6R1 for RACE f  
or mouse BSSP6 (reverse)

<400> 31  
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<210> 32  
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<210> 33  
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<220>  
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fy full-length mouse BSSP6-encoding mRNA (reverse)

<400> 33  
cggaattcgc attaagaaga ggttgag 28

<210> 34  
<211> 20  
<212> DNA  
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<220>  
<223> Designed oligonucleotide primer designated as hBSSP6R3 to amplify  
a portion of BSSP6 variant type-encoding mRNA from human prostat  
ic cancer cell line PC-3 (reverse)

<400> 34  
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<210> 35  
<211> 20  
<212> DNA  
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<220>

<223> Designed oligonucleotide primer designated as hBSSP6F7 to amplify  
a portion of human BSSP6-encoding mRNA (forward)

<400> 35

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20

<210> 36

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify conserved region of se  
rin proteases-encoding sequence

<220>

<221> misc\_feature

<222> (9)..(9)

<223> n is a, c, g or t.

<220>

<221> misc\_feature

<222> (12)..(12)

<223> n is a, c, g or t.

<400> 36

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20

<210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

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<220>

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<223> n is a, c, g or t.

<400> 37

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<210> 38

<211> 117

<212> DNA

<213> Artificial Sequence

<220>



<223> Designed oligonucleotide to construct plasmid pTrypHis

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<210> 39

<211> 117

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 39

gaattcggat ccttgatcatc gtcgtcatgg tgatgggtgat ggtgaaaggg ggcagcaaca 60  
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<210> 40

<211> 5

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<213> Artificial Sequence

<220>

<223> Synthetic

<400> 40

Asp Asp Asp Asp Lys  
1 5

<210> 41

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 41

Lys Val His Gly  
1